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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 07:23:35 ; Search time 92 Seconds

(without alignments)
425.532 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 190

Sequence: 1 MMNFQPPSKAMRASQMMTF.....HDGSLDLRSRRSVQEGNPRA 190

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 4

Total number of hits satisfying chosen parameters: 262137

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	330	4 Q9H8I7	Q9H8I7 homo sapien
2	39	20.5	757	11 Q9D4F1	Q9D4F1 mus musculu
3	8	4.2	335	17 Q9UXT5	Q9UXT5 pyrococcus
4	8	4.2	351	5 Q9XUX9	Q9XUX9 caenorhabdi
5	8	4.2	752	16 Q97KL3	Q97KL3 clostridium
6	7	3.7	148	6 Q95KK4	Q95KK4 oryctolagus
7	7	3.7	148	11 Q8R2K3	Q8R2K3 mus musculu
8	7	3.7	152	11 Q9CYR0	Q9CYR0 mus musculu
9	7	3.7	170	5 Q16583	Q16583 caenorhabdi
10	7	3.7	180	16 Q98QA6	Q98QA6 mycoplasma
11	7	3.7	202	16 Q92DQ9	Q92DQ9 listeria in
12	7	3.7	202	16 Q8Y8Y2	Q8Y8Y2 listeria mo
13	7	3.7	214	2 Q48599	Q48599 lactococcus
14	7	3.7	214	2 Q48637	Q48637 lactococcus
15	7	3.7	231	17 Q96XL5	Q96XL5 sulfolobus
16	7	3.7	244	2 Q50296	Q50296 anabaena va

17	7	3.7	244	16 Q57281	Q57281 anabaena sp
18	7	3.7	245	16 Q98R89	Q98R89 mycoplasma
19	7	3.7	251	8 Q47800	Q47800 gymnodraco
20	7	3.7	282	10 Q65045	Q65045 picea maria
21	7	3.7	298	2 Q8RS30	Q8RS30 comamonas a
22	7	3.7	324	17 Q29940	Q29940 archaeoglob
23	7	3.7	325	13 Q93259	Q93259 gallus gall
24	7	3.7	327	5 Q9XXA9	Q9XXA9 caenorhabdi
25	7	3.7	330	16 Q51564	Q51564 borrelia bu
26	7	3.7	335	2 Q9RLV9	Q9RLV9 listeria iv
27	7	3.7	338	16 Q8XDV8	Q8XDV8 escherichia
28	7	3.7	340	2 Q30478	Q30478 streptomyce
29	7	3.7	344	16 Q98KF2	Q98KF2 rhizobium 1
30	7	3.7	350	16 Q8RFH8	Q8RFH8 fuscobacteri
31	7	3.7	354	8 Q9MKL8	Q9MKL8 carabus abb
32	7	3.7	355	8 Q9MEG7	Q9MEG7 carabus opa
33	7	3.7	355	8 Q9MEG6	Q9MEG6 carabus opa
34	7	3.7	355	8 Q9MEC7	Q9MEC7 carabus gra
35	7	3.7	355	8 Q9ME44	Q9ME44 carabus arv
36	7	3.7	355	8 Q9ME14	Q9ME14 carabus por
37	7	3.7	355	8 Q9MDZ5	Q9MDZ5 carabus opa
38	7	3.7	355	8 Q9MDT2	Q9MDT2 carabus por
39	7	3.7	355	8 Q9MDT0	Q9MDT0 carabus gra
40	7	3.7	355	8 Q9MDS6	Q9MDS6 carabus por
41	7	3.7	355	8 Q9MDR6	Q9MDR6 carabus gra
42	7	3.7	355	8 Q9MDR4	Q9MDR4 carabus mun
43	7	3.7	355	8 Q9MDR3	Q9MDR3 carabus sch
44	7	3.7	355	8 Q9MDD3	Q9MDD3 carabus por
45	7	3.7	355	8 Q9MDB8	Q9MDB8 carabus opa

ALIGNMENTS

RESULT 1

Q9H8I7 ID Q9H8I7 PRELIMINARY; PRT; 330 AA.

AC Q9H8I7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ13533 fis, clone PLACE1009493.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiraori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Saito K.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Masuo Y.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEDO human cDNA sequencing project."
RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK023655; BAB14629.1; .
SQ SEQUENCE 330 AA; 38958 MW; EBA21A1AC1455C2E CRC64;

Query Match 100.0%; Score 190; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 6.6e-196;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMNFQPPSKAMRASQMMTFIFLFPSPFTGVLTATITWRLKPSADCGFRGLPLFIH 60
DB 141 MMNFQPPSKAMRASQMMTFIFLFPSPFTGVLTATITWRLKPSADCGFRGLPLFIH 200
QY 61 SIYSWIDTLSTRPGYLWVWVIYRNIGSVHFFILTLIVLIITVLYWQTEGRKIMIRLL 120
DB 201 SIYSWIDTLSTRPGYLWVWVIYRNIGSVHFFILTLIVLIITVLYWQTEGRKIMIRLL 260

QY 121 HEOIINEGDKMFLIEKLIKIDMEKANPSSLVLERREVEEQGFLHGEHDSLDLRSR 180
 |||||||
 Db 261 HEOIINEGDKMFLIEKLIKIDMEKANPSSLVLERREVEEQGFLHGEHDSLDLRSR 320
 QY 181 RSVQEGNPRA 190
 |||||||
 Db 321 RSVQEGNPRA 330

RESULT 2

Q9D4F1 PRELIMINARY; PRT; 757 AA.
 ID Q9D4F1
 AC Q9D4F1
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE 4932443108Rik protein.
 GN 4932443108Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL EMBL; AK016573; BAB30314.1;
 DR MGI:1921674; 4932443108Rik.
 SQ SEQUENCE 757 AA; 87667 MW; 320D61A71CF51DAE CRC64;

Query Match 20.5%; Score 39; DB 11; Length 757;
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

Q9UXT5 PRELIMINARY; PRT; 335 AA.
 ID Q9UXT5
 AC Q9UXT5
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical protein PAB1174.
 GN PAB1174.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]

Q9UXT5 PRELIMINARY; PRT; 335 AA.
 ID Q9UXT5
 AC Q9UXT5
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical protein PAB1174.
 GN PAB1174.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome
 structure and evolution."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ248288; CAB50678.1;
 DR InterPro; IPR005242; Cons_hypoth374.
 DR Pfam; PF03706; UPF0104; 1.
 DR TIGRFAMS; TIGR00374; TIGR00374; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 335 AA; 37288 MW; F29086681DAFCFF CRC64;

Query Match 4.2%; Score 8; DB 17; Length 335;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 ILTLIVLI 101
 |||||||
 Db 158 ILTLIVLI 165

RESULT 4

Q9XUX9 PRELIMINARY; PRT; 351 AA.
 ID Q9XUX9
 AC Q9XUX9
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE F57G4.4 protein.
 GN F57G4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

SEQUENCE FROM N.A.
 RA Ainscough R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81554; CAB04503.1;
 DR InterPro; IPR002900; DUF38.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF01827; DUF38; 1.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PSS0181; FBOX; 1.
 SQ SEQUENCE 351 AA; 40374 MW; 97F396F5BF82CA31 CRC64;

Query Match 4.2%; Score 8; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DGSIDLRS 179
 |||||||
 Db 55 DGSIDLRS 62

RESULT 5

Q97KL3 PRELIMINARY; PRT; 752 AA.
 ID Q97KL3
 AC Q97KL3
 DT 01-OCT-2001 (Tremblrel. 18, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE ATPase with chaperon activity, two ATP-binding domains, ClpC
 orthologs.

GN CAC0904.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007605; AAK78880.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003959; AAA_ATPase_cent.
DR InterPro: IPR01270; Chaprinin_c1pA/B.
DR Pfam: PF00004; AAA; 2.
DR PRINTS: PR00300; CLPPROTEASEA.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00871; CLPAB_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 752 AA; 84925 MW; 57B4C4B6C47D80A6 CRC64;

Query Match 4.2%; Score 8; DB 16; Length 752;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 IINEGKDK 131
|||||
Db 678 IINEGKDK 685

RESULT 6
O95KR4 PRELIMINARY; PRT; 148 AA.
ID O95KR4;
AC O95KR4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Single-stranded DNA binding precursor.
GN SSB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Dufresne C., Gueride M.;
RT "Identification and expression of cDNA and pseudogene coding for the
RT rabbit mitochondrial single-strand DNA-binding protein.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ311162; CAC38115.1; -.
DR InterPro: IPR000424; SSB_protein.
DR Pfam: PF00436; SSB; 1.
DR TIGRfams: TIGR00621; ssb; 1.
DR PROSITE: PS00735; SSB_1; UNKNOWN_1.
DR PROSITE: PS00736; SSB_2; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 148 POTENTIAL.
SQ SEQUENCE 148 AA; 17155 MW; 9AF894B64686C43 CRC64;

Query Match 3.7%; Score 7; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLYER 157
|||||
Db 22 SSVLYER 28

RESULT 7
O8R2K3 PRELIMINARY; PRT; 148 AA.
ID O8R2K3;
AC O8R2K3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to single-stranded DNA binding protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028648; AAH28648.1; -.
SQ SEQUENCE 148 AA; 17157 MW; E5C00016DF6B4CD CRC64;

Query Match 3.7%; Score 7; DB 11; Length 148;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLYER 157
|||||
Db 22 SSVLYER 28

RESULT 8
O9CYR0 PRELIMINARY; PRT; 152 AA.
ID O9CYR0;
AC O9CYR0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 2810480P10R1k protein.
GN 2810480P10R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seyer T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK013425; BAB28850.1; -.
DR HSSP: Q04837; 3UL.
DR MGD: MGI:1920040; 2810480P10R1k.
DR InterPro: IPR000424; SSB_protein.
DR Pfam: PF00436; SSB; 1.

DR TIGR00621; ssb; 1.
DR PROSITE; PS00735; SSB_1; 1.
DR PROSITE; PS00736; SSB_2; 1.
SO SEQUENCE 152 AA; 17319 MW; 719B9F03C4C0D1EE CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 11; Length 152;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 SSVLER 157
Db 22 SSVLER 28

RESULT 9

016583 PRELIMINARY; PRT; 170 AA.
AC 016583;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 19.8 kDa protein.
GN C33C12.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Gattung S., Scheet P.;
RT "The sequence of C. elegans cosmid C33C12.";
RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF016662; AAB66062.1; .
KW Hypothetical protein.

SO SEQUENCE 170 AA; 19762 MW; D6C3E6F4BEDE52D0 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 5; Length 170;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 FLIEKLI 139
Db 56 FLIEKLI 62

RESULT 10

0980A6 PRELIMINARY; PRT; 180 AA.
AC 0980A6;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Hypothetical protein MYPV_4600.
GN MYPV_4600.

OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UAB CTIP;
RX MEDLINE-21267165; PubMed-11353084;
RA Chamblaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445564; CAC13633.1; .
DR Mypulist; MYPV_4600; .

KW Hypothetical protein; Complete proteome.
SO SEQUENCE 180 AA; 20466 MW; 6BA8C675358D167B CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 16; Length 180;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 IEKLIK 141
Db 142 IEKLIK 148

RESULT 11

092D09 PRELIMINARY; PRT; 202 AA.
AC 092D09;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein lin0754.
GN LIN0754.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.

OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / SEROVAR 6A;
RX PubMed-11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusnock C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutlian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596166; CAC95986.1; .
DR Lislilist; LIN00754; .
DR InterPro; IPR000379; Ser_estrs_site.

KW Hypothetical protein; Complete proteome.
SO SEQUENCE 202 AA; 22393 MW; 8A47B5C8D300D56E CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 16; Length 202;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 HDGSIDL 177
Db 62 HDGSIDL 68

RESULT 12

08Y8Y2 PRELIMINARY; PRT; 202 AA.
ID 08Y8Y2
AC 08Y8Y2;

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical protein lmo0760.
 GN LMO0760.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EGD-E / SEROVAR 1/2A;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
 Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL: AL591976; CAC98838.1; -
 DR Listlist; LMO00760; -
 DR InterPro: IPR000379; Ser_estrs_site.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 202 AA; 22264 MW; 37CE2E2A872E347 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 7; DB 16; Length 202;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 171 HDGSIDL 177
 Db 62 HDGSIDL 68

RESULT 13
 Q48599
 ID Q48599 PRELIMINARY; PRT; 214 AA.
 AC Q48599;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE NISG.
 GN NISG.
 OS Lactococcus lactis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-6F3;
 RX MEDLINE=95314241; PubMed=7793910;
 RA Siegers K., Entian K.D.;
 RT "Genes involved in immunity to the lantibiotic nisin in Lactococcus
 lactis 6F3.";
 RL Appl. Environ. Microbiol. 61:1082-1089(1995).
 DR EMBL: U17255; AAC43329.1; -
 SQ SEQUENCE 214 AA; 24193 MW; 1648256FC07C9A85 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 7; DB 2; Length 214;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 FLFFPS 28
 Db 96 FLFFPS 102

RESULT 14
 Q48637
 ID Q48637 PRELIMINARY; PRT; 214 AA.
 AC Q48637;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Membrane protein.
 GN NISG.
 OS Lactococcus lactis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452385; PubMed=10524754;
 RA Immonen T., Saris P.E.J.;
 RT "Characterization of the nisFG operon of the nisin Z producing
 RT Lactococcus lactis subsp. lactis N8 strain.";
 RL DNA Seq. 9:263-274(1998).
 DR EMBL: Z29363; CAA82549.1; -
 SQ SEQUENCE 214 AA; 24174 MW; 8C28257F1A10B2F9 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 7; DB 2; Length 214;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 FLFFPS 28
 Db 96 FLFFPS 102

RESULT 15
 Q96XL5
 ID Q96XL5 PRELIMINARY; PRT; 231 AA.
 AC Q96XL5;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hypothetical protein ST2501.
 GN ST2501.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takanashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagil M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000990; BAB67612.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 231 AA; 26846 MW; F59852E1099E7CD1 CRC64;

Query Match
 Best Local Similarity 3.7%; Score 7; DB 17; Length 231;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 IINEGKD 130
 Db 223 IINEGKD 229

RESULT 16

050296
ID 050296 PRELIMINARY; PRT: 244 AA.
AC 050296;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ATP-binding subunit.
GN DEVA.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29413;
RX MEDLINE=98440130; PubMed=9767151;
RA Fiedler G., Arnold M., Maldener I.;
RT "Sequence and mutational analysis of the devBCA gene cluster encoding a putative ABC transporter in the cyanobacterium Anabaena variabilis
RT ATCC 29413."
RL Blochlm. Biophys. Acta 1375:140-143(1998).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: AJ003195; CAA05977.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00005; ABC_tran; 1.
DR PRODOM: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Transport.
SQ SEQUENCE 244 AA; 26709 MW; 7854524E915B6D20 CRC64;

Query Match 3.7%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RSVQEGN 187
Db 60 RSVQEGN 66

RESULT 17
057281
ID 057281 PRELIMINARY; PRT: 244 AA.
AC 057281;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE PCC7120 DEVB, DEVC, DEVA genes, ORF2 & ORF3 (Heterocyst specific
DE ABC-transporter, ATP-binding subunit).
GN DEVA OR ALR3712.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC7120;
RA Fiedler G., Arnold M., Maldener I.;
RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PASTEUR C NO. 7120;
RX MEDLINE=95095923; PubMed=8002578;
RA Maldener I., Fiedler G., Ernst A., Fernandez-Pinas F., Wolk C.P.;
RT "Characterization of devA, a gene required for the maturation of
RT proheterocysts in the cyanobacterium Anabaena sp. strain PCC 7120."
RL J. Bacteriol. 176:7543-7549(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: X99672; CAA67987.1; -.
DR EMBL: X75422; CAA53174.1; -.
DR EMBL: AP003594; BAB75411.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00005; ABC_tran; 1.
DR PRODOM: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 244 AA; 26723 MW; 34182185A65C0A4B CRC64;

Query Match 3.7%; Score 7; DB 16; Length 244;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RSVQEGN 187
Db 60 RSVQEGN 66

RESULT 18
098R89
ID 098R89 PRELIMINARY; PRT: 245 AA.
AC 098R89;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE Hypothetical protein MYPV_1210.
GN MYPV_1210.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CUP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL: AL445563; CAC13294.1; -.
DR MYPULIST: MYPV_1210; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 245 AA; 28756 MW; 54D4EA7AFCF21B29 CRC64;

Query Match 3.7%; Score 7; DB 16; Length 245;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 TLIVLII 102
Db 223 TLIVLII 229

RESULT 19
047800
ID 047800 PRELIMINARY; PRT: 251 AA.
AC 047800;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Gymnodraco acuticeps (Antarctic dragonfish).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Notothenioidae; Bathyaconidae; Gymnodraco.
 OX NCBI_TaxID=8218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Chen W.J., Bonillo C., Lecointre G.;
 RT "Phylogeny of the Chanichthyidae (Notothenioidae, Teleostei) based on
 RT two mitochondrial genes.";
 RL (in) di Prisco G., Pisano E., Clarke A. (eds.);
 RL FISHES OF ANTARCTICA. A BIOLOGICAL OVERVIEW, pp.1-1,
 RL Springer-Verlag Publishers (1998).
 CC -1- FUNCTION: COMPONENT OF THE UBIOUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC EMBL: AF037109; AAC04790.1; -.
 DR InterPro: IPR001179; CYL_b_b6.
 DR Pfam: PF00032; cytochrome_b_c1.
 DR Pfam: PF00033; cytochrome_b_n; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KM Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 251 251
 SQ SEQUENCE 251 AA; 27682 MW; A9B974A9B9484B11 CRC64;

Query Match 3.7%; Score 7; DB 8; Length 251;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21 IFLFFP 27
 Db 235 IFLFFP 241

RESULT 20
 O65045
 ID O65045 PRELIMINARY; PRT; 282 AA.
 AC O65045;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Probable aquaporin.
 GN SB01.
 OS Picea mariana (black spruce).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 OX NCBI_TaxID=3335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98278823; PubMed=9611216;
 RA Perry D.J., Bousquet J.;
 RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,
 RT characterization and analysis of linkage in black spruce.";
 RL Genetics 149:1089-1098(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
 DR EMBL: AF051202; AAC32107.1; -.
 DR HSSP: P29972; IFOY.
 DR InterPro: IPR000425; MIP_family.
 DR Pfam: PF00230; MIP; 1.
 DR PRINTS: PRO0783; MINTINSICP.
 DR PRODOM: PD000295; MIP_family; 1.
 DR TIGRfams: TIGR00861; MIP; 1.

DR PROSITE: PS00221; MIP; 1.
 KW Porin; Transmembrane; Transport.
 SQ SEQUENCE 282 AA; 30154 MW; 89204AACAA9D8340 CRC64;
 Query Match 3.7%; Score 7; DB 10; Length 282;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 159 EVEQGF 165
 Db 8 EVEQGF 14

RESULT 21
 O8RS30
 ID O8RS30 PRELIMINARY; PRT; 298 AA.
 AC O8RS30;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ORF5.
 GN ORF5.
 OS Comamonas acidovorans (Pseudomonas acidovorans).
 OC Plasmid puoh1.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Delftia.
 OX NCBI_TaxID=80866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B;
 RA Sota M., Endo M., Nitta K., Kawasaki H., Tsuda M.;
 RT "Characterization of a class II defective transposon carrying two
 RT halacetate dehalogenase genes from Delftia acidovorans plasmid
 RT puoh1.";
 RL Appl. Environ. Microbiol. 0:0-0(2002).
 DR EMBL: AB049198; BAB85587.1; -.
 KW Plasmid.
 SQ SEQUENCE 298 AA; 32798 MW; 8FC1102E7A7EE17 CRC64;

Query Match 3.7%; Score 7; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 178 RSRSVQ 184
 Db 52 RSRSVQ 58

RESULT 22
 O29940
 ID O29940 PRELIMINARY; PRT; 324 AA.
 AC O29940;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE UDP-glucose dehydrogenase (UGD-1).
 GN AF0302.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon *Archaeoglobus fulgidus*.";
RL Nature 390:364-370(1997).
DR EMBL; AE001084; AAB90929.1; -.
DR TIGR; AF0302; -.
DR InterPro; IPR001732; UDPG_MGDP_dh.
DR Pfam; PF00984; UDPG_MGDP_dh; 1.
DR Pfam; PF03721; UDPG_MGDP_dh_N; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 324 AA; 35838 MW; 36D058B58C00B08 CRC64;

Query Match 3.7%; Score 7; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DGSLLDR 178
Db 89 DGSLLDR 95
|||||

RESULT 23
ID 093259 PRELIMINARY; PRT; 325 AA.
AC 093259;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Melanocortin 3-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=99144114; Pubmed=9990303;
RA Takeuchi S., Takahashi S.;
RT "A possible involvement of melanocortin 3-receptor in the regulation
RT of adrenal gland function in the chicken.";
RL Biochim. Biophys. Acta 1448:512-518(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB017137; BAA32555.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 325 AA; 36601 MW; 94FA6631ED144C17 CRC64;

Query Match 3.7%; Score 7; DB 13; Length 325;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LTLIVLI 101
Db 162 LTLIVLI 168
|||||

RESULT 24
ID 09XXA9 PRELIMINARY; PRT; 327 AA.
AC 09XXA9;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Y94A7B.5 protein.
GN Y94A7B.5.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RT none;
RT "Genome sequence of the nematode *C.elegans*: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL023856; CAA19567.1; -.
DR InterPro; IPR003003; 7TM_chemo2.
DR InterPro; IPR000168; 7TM_nematode.
DR Pfam; PF01604; 7tm_5; 1.
SQ SEQUENCE 327 AA; 37108 MW; B251B168CC77BBBD CRC64;

Query Match 3.7%; Score 7; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LTLIVLI 101
Db 197 LTLIVLI 203
|||||

RESULT 25
ID 051564 PRELIMINARY; PRT; 330 AA.
AC 051564;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein BB0619.
GN BB0619.
OS *Borrelia burgdorferi* (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; *Borrelia*.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; Pubmed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Matthey L., McDonald L., Artlisch P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, *Borrelia*
RT *burgdorferi*.";
RL Nature 390:580-586(1997).
DR EMBL; AE001163; AAC66977.1; -.
DR TIGR; BB0619; -.
DR InterPro; IPR003156; DHHA1.
DR InterPro; IPR001667; Psesterase.
DR Pfam; PF01368; DHH; 1.
DR Pfam; PF02272; DHHA1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 330 AA; 37377 MW; 392DB8DF6160DEA6 CRC64;

Query Match 3.7%; Score 7; DB 16; Length 330;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 FLIEKLI 139
Db 139 FLIEKLI 145
|||||

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RESULT 26
O9RLV9          PRELIMINARY;      PRT;      335 AA.
AC  O9RLV9;
DT  01-MAY-2000 (TReMBLrel. 13, Created)
DT  01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE  01-JUN-2002 (TReMBLrel. 21, Last annotation update)
OS  Sphingomyelinase-c.
OC  Listeria ivanovii.
OC  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OX  Listeriaceae; Listeria.
RN  NCBI_TaxID=1638;
RP  [1]
RC  SEQUENCE FROM N.A.
RX  STRAIN=ATCC 19119;
RX  MEDLINE=99348382; PubMed=10417642;
RA  Gonzalez-Zorn B., Dominguez-Bernal G., Suarez M., Ripio M.T., Vega Y.,
RA  Novella S., Vazquez-Boland J.A.;
RT  "The smcl gene of Listeria ivanovii encodes a sphingomyelinase C that
RT  mediates bacterial escape from the phagocytic vacuole.";
RL  Mol. Microbiol. 33:510-523(1999).
DR  EMBL; Y09477; CAA70683.2; -.
DR  InterPro; IPR005135; Exo_endo_phos.
DR  Pfam; PF03372; Exo_endo_phos; 1.
SQ  SEQUENCE 335 AA; 38455 MW; 46F398E58A8434D7 CRC64;

Query Match      3.7%; Score 7; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  20 FIFLFF 26
    |||||
DB  17 FIFLFF 23

RESULT 27
O8XDV8          PRELIMINARY;      PRT;      338 AA.
AC  O8XDV8;
DT  01-MAR-2002 (TReMBLrel. 20, Created)
DT  01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE  01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE  Periplasmic binding protein component of Pn transporter.
GN  PHND OR 25707 OR ECS5087.
OS  Escherichia coli O157:H7.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX  Escherichia.
RN  NCBI_TaxID=83334;
RP  [1]
RC  SEQUENCE FROM N.A.
RX  STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX  MEDLINE=21074935; PubMed=11206551;
RA  Perina N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA  Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA  Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA  Grobeck E.J., Davis N.W., Iam A., Dimalanta E.T., Potamousis K.,
RA  Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA  Welch R.A., Blattner F.R.;
RT  "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL  Nature 409:529-533(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=O157:H7 / RIMD 0509952;
RX  MEDLINE=21156231; PubMed=11258796;
RA  Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA  Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA  Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA  Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT  "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT  O157:H7 and genomic comparison with a laboratory strain K-12.";
RL  DNA Res. 8:11-22(2001).
DR  EMBL; AE005643; AAG59304.1; -.
DR  EMBL; AP002568; BAB38510.1; -.

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KW  Complete proteome.
SQ  SEQUENCE 338 AA; 37418 MW; A6AFC8CFF4C9D6B5 CRC64;

Query Match      3.7%; Score 7; DB 16; Length 338;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  141 LQDMEK 147
    |||||
DB  54 LQDMEK 60

RESULT 28
O30478          PRELIMINARY;      PRT;      340 AA.
AC  O30478;
DT  01-JAN-1998 (TReMBLrel. 05, Created)
DT  01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DE  01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE  Putative pteridine-dependent dioxigenase.
OS  Streptomyces hygroscopicus.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1912;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 29253;
RX  MEDLINE=98085969; PubMed=9426000;
RA  Ruan X., Stassi D., Lax S.A., Katz L.;
RT  "A second type-I PKS gene cluster isolated from Streptomyces
RT  hygroscopicus ATCC 29253, a rapamycin-producing strain.";
RL  Gene 203:1-9(1997).
DR  EMBL; AF007101; AAC38060.1; -.
DR  InterPro; IPR000543; Yj9F-like.
DR  Pfam; PF01042; UPR0076; 1.
KW  Dioxigenase.
SQ  SEQUENCE 340 AA; 37429 MW; 74B9440290366D8B CRC64;

Query Match      3.7%; Score 7; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  149 NPSSLVL 155
    |||||
DB  2 NPSSLVL 8

RESULT 29
O98KF2          PRELIMINARY;      PRT;      344 AA.
AC  O98KF2;
DT  01-OCT-2001 (TReMBLrel. 18, Created)
DT  01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DE  01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE  Permease protein of ribose ABC transporter.
GN  MLL1505.
OS  Rhizobium loti (Mesorhizobium loti).
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Phyllobacteriaceae; Mesorhizobium.
OX  NCBI_TaxID=381;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MAFF303099;
RX  MEDLINE=21082930; PubMed=11214968;
RA  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA  Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA  Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA  Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA  Takeuchi C., Yamada M., Tabata S.;
RT  "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT  Mesorhizobium loti.";
RL  DNA Res. 7:331-338(2000).
DR  EMBL; AP002997; BAB48862.1; -.

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DR InterPro; IPR001851; Bac_inmem_transp.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF02653; BPD_transp_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 344 AA; 36981 MW; AE4A9A22DD070150 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 16; Length 344;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 QIINEGK 129
Db 162 QIINEGK 168

RESULT 30
Q8RFH8 ID Q8RFH8 PRELIMINARY; PRT; 350 AA.
AC Q8RFH8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical cytosolic protein FN0719.
GN FN0719.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=1189109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fongstein M., Kyriades N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010582; AAL94915.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 350 AA; 41804 MW; 21A901CF46CD50D8 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 16; Length 350;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 LIEKLIK 140
Db 335 LIEKLIK 341

RESULT 31
Q9MKL8 ID Q9MKL8 PRELIMINARY; PRT; 354 AA.
AC Q9MKL8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus abbreviatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=114446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F;
RA Prueser F., Brueckner M., Mossakowski D.;
RT "Colonization of Canary Islands by Carabus species: evidence from

RT different character complexes.";
RL (In) Brandmayr P., Lovel G., Brandmayr T.Z., Casale A.,
RL Vigna Taglianti A. (eds.);
RL Natural history and applied ecology of carabid beetles (Proceedings of
RL the 9th European carabidologist meeting), pp.1-1, Pensoft.
RL Sofia (2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF231695; AAF61942.1; -;
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 354 AA; 40667 MW; B0AE2E15FF5396C2 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 354;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 32
Q9MEG7 ID Q9MEG7 PRELIMINARY; PRT; 355 AA.
AC Q9MEG7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomlinaga O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RT from mitochondrial ND5 gene sequences."
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB039808; BAA92457.1; -;
DR EMBL; AB039804; BAA92453.1; -;
DR EMBL; AB039805; BAA92454.1; -;
DR EMBL; AB039806; BAA92455.1; -;
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40947 MW; 0556E113E1D97D80 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 33
Q9MEG6 ID Q9MEG6 PRELIMINARY; PRT; 355 AA.
AC Q9MEG6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).

```
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomioka O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomiocarabus opaculus (Coleoptera, Carabidae) as deduced
RL from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB039809; BAA92458.1; -.
DR EMBL: AB039807; BAA92456.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40961 MW; 0556E113FF289280 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 34
O9MEC7 PRELIMINARY; PRT; 355 AA.
ID O9MEC7;
AC O9MEC7;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus granulatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RL tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OH33;
RA Sota T., Vogler A.P.;
RT "Incongruence of mitochondrial and nuclear gene trees in the carabid
RL beetles Ohomopterus.";
RL Syst. Biol. 0:0-0(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB041069; BAA94628.1; -.
DR EMBL: AF219473; AAF62460.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40873 MW; 1AFA4B4EA9BA16BA CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 100.0%; Pred. No. 68;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 35
O9ME44 PRELIMINARY; PRT; 355 AA.
ID O9ME44;
AC O9ME44;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus arvensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=49192;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35, 31, 33, 36, AND 34; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RL tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL: AB041059; BAA94618.1; -.
DR EMBL: AB041054; BAA94613.1; -.
DR EMBL: AB041056; BAA94615.1; -.
DR EMBL: AB041057; BAA94616.1; -.
DR EMBL: AB041058; BAA94617.1; -.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40824 MW; 5401A867989B3D75 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 36
O9ME14 PRELIMINARY; PRT; 355 AA.
ID O9ME14;
AC O9ME14;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis porrecticollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87295;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37, 33, 34, AND 36; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomioka O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RL (Coleoptera, Carabidae) in the Japanese Islands inferred from
RT Mitochondrial ND5 Gene Sequences.";
```

RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB022580; BAA74502.1; -.
DR EMBL; AB022586; BAA74498.1; -.
DR EMBL; AB022587; BAA74499.1; -.
DR EMBL; AB022589; BAA74501.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40914 MW; 67A294D3AE3C4B30 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 37
Q9MDT5 PRELIMINARY; PRT; 355 AA.
ID Q9MDT5
AC Q9MDT5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOKKAIDO-NITKAPP08, AND HOKKAIDO-SAROMA3; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomimaga O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RT from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB039800; BAA92449.1; -.
DR EMBL; AB039796; BAA92445.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40899 MW; 704B4C5FBCA13D00 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 38
Q9MDT2 PRELIMINARY; PRT; 355 AA.
ID Q9MDT2
AC Q9MDT2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis kansaiensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23, AND 22; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomimaga O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands Inferred from
RT Mitochondrial ND5 Gene Sequences.";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB022576; BAA74488.1; -.
DR EMBL; AB022575; BAA74487.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40944 MW; 8A2E3165B68D5F10 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 39
Q9MDT0 PRELIMINARY; PRT; 355 AA.
ID Q9MDT0
AC Q9MDT0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus granulatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=45, 43, AND 39; TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomimaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna Inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041073; BAA94632.1; -.
DR EMBL; AB041070; BAA94629.1; -.
DR EMBL; AB041071; BAA94630.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40803 MW; 8BC0FE5FFB605A0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 40
Q9MDS6

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ID Q9MDS6 PRELIMINARY; PRT; 355 AA.
AC Q9MDS6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis kansalensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomioka O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands inferred from
RT Mitochondrial ND5 Gene Sequences.";
RT Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB022585; BAA74497.1; -.
DR EMBL; AB022571; BAA74483.1; -.
DR EMBL; AB022573; BAA74485.1; -.
DR EMBL; AB022574; BAA74486.1; -.
DR EMBL; AB022577; BAA74489.1; -.
DR EMBL; AB022578; BAA74490.1; -.
DR EMBL; AB022579; BAA74491.1; -.
DR EMBL; AB022580; BAA74492.1; -.
DR EMBL; AB022581; BAA74493.1; -.
DR EMBL; AB022582; BAA74494.1; -.
DR EMBL; AB022583; BAA74495.1; -.
DR EMBL; AB022584; BAA74496.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT SEQUENCE 355 AA; 40914 MW; 8D548DA4BAF52A11 CRC64;
SQ

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 41
Q9MDR6 PRELIMINARY; PRT; 355 AA.
AC Q9MDR6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus granulatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118799;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=49, AND 47; TISSUE=THORAX MUSCLE;
RC MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RT J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
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DR EMBL; AB041067; BAA94626.1; -.
DR EMBL; AB041066; BAA94625.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT SEQUENCE 355 AA; 40860 MW; 927E920321AE5665 CRC64;
SQ

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 42
Q9MDR4 PRELIMINARY; PRT; 355 AA.
AC Q9MDR4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus munakatal.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=120937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THORAX MUSCLE;
RC MEDLINE=20296815; PubMed=10835484;
RA Tomioka O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RT J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041084; BAA94643.1; -.
DR EMBL; AB041083; BAA94642.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT SEQUENCE 355 AA; 40895 MW; 956C1181F08A06FF CRC64;
SQ

Query Match 3.7%; Score 7; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
DB 157 FIFLFF 163

RESULT 43
Q9MDR3 PRELIMINARY; PRT; 355 AA.
AC Q9MDR3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus schrenckii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=120935;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THORAX MUSCLE;
RX MEDLINE=20296815; PubMed=10835484;
RA Tomimaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
RT "Formation of the Japanese Carabina Fauna inferred from a phylogenetic
RT tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
RL J. Mol. Evol. 50:541-549(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB041081; BAA94640.1; -
DR EMBL; AB041080; BAA94639.1; -
DR InterPro; IPR001750; Oxidored_q1.
DR pfam; PF00361; oxidored_q1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40868 MW; 977A20EC3532FD9C CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLFF 26
Db 157 FIFLFF 163

RESULT 44
Q9MD3 PRELIMINARY; PRT; 355 AA.
ID Q9MD3:
AC Q9MD3:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus porrecticollis porrecticollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=87295;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12, 1, 2, 3, 4, 5, 6, 9, 10, AND 11; TISSUE=THORAX MUSCLE;
RA Kim C.G., Tomimaga O., Su Z.H., Osawa S.;
RT "Origin and Diversification of Euleptocarabus porrecticollis
RT (Coleoptera, Carabidae) in the Japanese Islands inferred from
RT Mitochondrial ND5 Gene Sequences.";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB022565; BAA74477.1; -
DR EMBL; AB022555; BAA74467.1; -
DR EMBL; AB022556; BAA74468.1; -
DR EMBL; AB022557; BAA74469.1; -
DR EMBL; AB022558; BAA74470.1; -
DR EMBL; AB022559; BAA74471.1; -
DR EMBL; AB022560; BAA74472.1; -
DR EMBL; AB022562; BAA74474.1; -
DR EMBL; AB022563; BAA74475.1; -
DR EMBL; AB022564; BAA74476.1; -
DR InterPro; IPR001750; Oxidored_q1.
DR pfam; PF00361; oxidored_q1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40916 MW; E6B39DF6723A8FEB CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 45
Q9MDB8 PRELIMINARY; PRT; 355 AA.
ID Q9MDB8:
AC Q9MDB8:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Carabus opaculus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
OC Carabus.
OX NCBI_TaxID=118064;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOKKAIDO-KUSHIRO2, AND HOKKAIDO-NEMURO1; TISSUE=THORAX MUSCLE;
RA Su Z.H., Tomimaga O., Saito S., Kim C.G., Osawa S.;
RT "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
RT from mitochondrial ND5 gene sequences.";
RL Elytra 28:13-20(2000).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AB039795; BAA92444.1; -
DR EMBL; AB039794; BAA92443.1; -
DR InterPro; IPR001750; Oxidored_q1.
DR pfam; PF00361; oxidored_q1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40959 MW; F071F1D770E4FED4 CRC64;

Query Match
Best Local Similarity 3.7%; Score 7; DB 8; Length 355;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: November 9, 2002, 07:30:24
Job time : 95 secs